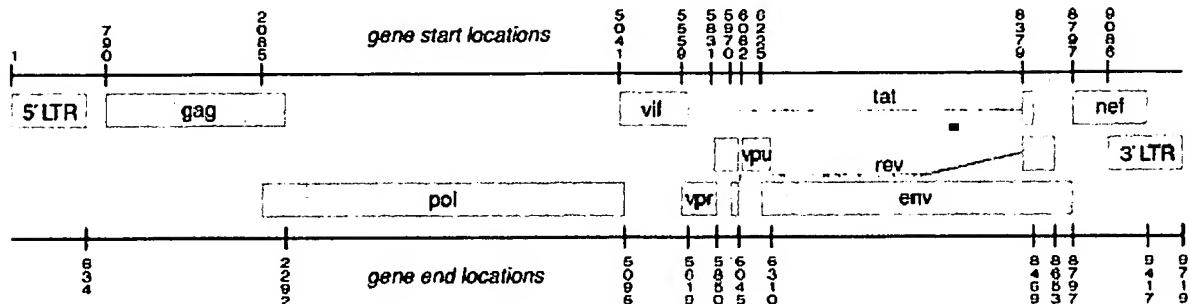


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MAb_ID 5F3
HXB2_Location gp160(525-543) [gp160_Epitope_Map](#)
Author_Location gp41(526-543 BH10)
Research_Contact H. Katinger, Inst. Appl. Microbiol., Vienna, Austria
Epitope AAGSTMGAASMTLTVQARQ [Epitope_Alignment](#)
Ab_Type
Neutralizing no
Species (Isotype) human(IgG1κ)
Immunogen HIV-1 infection
Keywords

Notes

- 5F3: This epitope is similar to a fragment of the HLA class II histocompatibility antigen, GGSCMAALTIVTLTV. [Maksiutov2002](#)
- 5F3: Human MAb generated by electrofusion of PBL from HIV-1+ volunteers with CB-F7 cells. [Buchacher1994](#)

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MAb_ID 25C2 (IAM 41-25C2)
HXB2_Location gp160(525-543) [gp160_Epitope_Map](#)
Author_Location gp41(526-543 BH10)

Research_Contact H. Katinger, Inst. Appl. Microbiol., Vienna, Austria and Viral Testing Systems, Houston, TX

Epitope AAGSTMGAASMTLTVQARQ

Epitope_Alignment

Ab_Type

Neutralizing no

Species_(Isotype) human(IgG1κ)

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Displaying record number 740

MAb_ID 24G3

HXB2_Location gp160(525-543) gp160_Epitope_Map

Author_Location gp41(526-543 BH10)

Research_Contact H. Katinger, Inst. Appl. Microbiol., Vienna, Austria

Epitope AAGSTMGAASMTLTVQARQ Epitope_Alignment

Ab_Type

Neutralizing no

Species (Isotype) human(IgG1κ)

Immunogen HIV-1 infection

Keywords

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MAb_ID 1A1

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Author_Location gp41(526-543 BH10)

Research_Contact H. Katinger, Inst. Appl. Microbiol., Vienna, Austria

Epitope AAGSTMGAASMTLTVQARQ [Epitope_Alignment](#)

Ab_Type

Neutralizing no

Species (Isotype) human(IgG1κ)

Immunogen HIV-1 infection

Keywords

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Author_Location gp41(526-543 BH10)

Research_Contact H. Katinger, Inst. Appl. Microbiol., Vienna, Austria

Epitope AAGSTMGAASMTLTVQARQ [Epitope_Alignment](#)

Ab_Type

Neutralizing no

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<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: primer
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20

A G C A G C A G C A A G C A C T A T G
A A G S T M |

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SSRKHYX

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>seq1
SSRKHYX
>seq1
XAAGSTMX.
>seq1
XQQEALW
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determination of the DNA concentration at 260 nm in a spectrophotometer (Beckman), sequenced by the Sanger method (F. Sanger, Proc. Natl. Acad. Sci., 74: 5463, 1977). Instead of sequencing with Klenow DNA polymerase, the sequencing reaction was carried out using a kit from Applied Biosystems ("Taq dye deoxy terminator cycle sequencing", order No.: 401150). Primer 1 (SEQ ID NO:35) or primer 2 (SEQ ID NO:36) (in each case 1 μ M) was employed as primers in separate sequencing reactions. The sequencing reaction was analysed on a 373A DNA sequencing apparatus (Applied Biosystems) in accordance with the instructions of the apparatus manufacturer.

[064] The nucleotide sequence of the amplified DNA region, and the amino acid sequence deduced from it, are presented in Table 1. Table 1 includes the DNA sequences SEQ ID NO:37 and SEQ ID NO:38, as well as amino acid SEQ ID NO:39. The top line in Table 1 corresponds to SEQ ID NO:37, the middle line corresponds to SEQ ID NO:38, and the bottom line corresponds to the amino acid SEQ ID NO:39.

[065] Table 1:

```

GCAGCAGCGGCAACAGCGCTGACGGTACGGACCCACAGTGTACTGAAGGGTATAGTCAAC
-----+-----+-----+-----+-----+-----+-----+-----+
CGCGTCGCCGTTGTCGCGACTGCCATGCCCTGGGTGTACATGACTTCCCATATCACGTTG
A A A T A L T V R T H S V L K G I V Q Q
AGCAGGACAACCTGCTGAGAGCGATAACAGGCCAGCAACACTTGCTGAGGTTATCTGTAT
-----+-----+-----+-----+-----+-----+-----+-----+
TCGTCCCTGTTGGACGACTCTCGCTATGTCCGGGTGTTGTGAACGACTCCAATAGACATA
Q D N L L R A I Q A Q Q H L L R L S V W

```

infected with MVP-5180/91 (SEQ ID NO:56) were pipetted into a 100 μ l reaction mixture (0.25 mM dNTP, in each case 1 μ m primer 1 and primer 2; 10 mM Tris HCl, pH 8.3, 50 mM KCl, 1.5 MgCl₂, 0.001% gelatin, 2.5 units of Taq polymerase (Perkin Elmer)), and amplification was then carried out in accordance with the following temperature program: 1. initial denaturation: 3' 95°C, 2. amplification: 90" 94°C, 60" 56°C, 90", 72°C (30 cycles).

[062] The primers used for the PCR and for nucleotide sequencing were synthesized on a Biosearch 8750 oligonucleotide synthesizer.

Primer 1 (SEQ ID NO:35): AGC AGC AGG AAG CAC TAT GG
(coordinates from HIV-1 isolate HXB2: bases 7795-7814,
corresponds to primer sk 68) (SEQ ID NO:21)

Primer 2 (SEQ ID NO:36): GAG TTT TCC AGA GCA ACC CC
(coordinates from HIV-1 isolate HXB2: bases 8003-8022,
corresponds to primer env b (SEQ ID NO:20).

[063] The amplified DNA was fractionated on a 3% "Nusieve" agarose gel (from Biozyme) and the amplified fragment was then cut out and an equal volume of buffer (1 * TBE (0.09 M Tris borate, 0.002 M EDTA, pH 8.0) was added to it. After incubating the DNA/agarose mixture at 70°C for 10 minutes, and subsequently extracting with phenol, the DNA was precipitated from the aqueous phase by adding 1/10 vol of 3 M NaAc, pH 5.5, and 2 vol of ethanol and storing at -20°C for 15', and then subsequently pelleted in a centrifuge (Eppendorf) (13,000 rpm, 10', 4°C). The pelleted DNA was dried and taken up in water, and then, after photometric



US00515694A

United States Patent [19]

Luciw et al.

[11] Patent Number: **5,156,949**[45] Date of Patent: **Oct. 20, 1992**

[54] **IMMUNOASSAYS FOR ANTIBODY TO HUMAN IMMUNODEFICIENCY VIRUS USING RECOMBINANT ANTIGENS**

[75] Inventors: Paul A. Luciw, Davis; Dino Dina, San Francisco, both of Calif.

[73] Assignee: Chiron Corporation, Emeryville, Calif.

[21] Appl. No.: 138,894

[22] Filed: Dec. 24, 1987

Related U.S. Application Data

[63] Continuation-in-part of Ser. No. 773,447, Sep. 6, 1985, abandoned, which is a continuation-in-part of Ser. No. 696,534, Jan. 30, 1985, abandoned, which is a continuation-in-part of Ser. No. 667,501, Oct. 31, 1984, abandoned.

[51] Int. Cl.⁵ G01N 33/53; C12P 21/06; C12N 15/00; C12N 1/20

[52] U.S. Cl. 435/5; 435/7.2; 435/69.1; 435/172.3; 435/252.33; 435/810; 435/820; 435/974; 935/60; 935/66; 935/69; 935/71

[58] Field of Search 435/5, 7, 68, 172.3, 435/235-239, 810, 820, 948, 69.1, 974; 935/60, 81, 66, 69, 71

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(List continued on next page.)

Primary Examiner—Christine M. Nucker*Assistant Examiner*—M. P. Woodward*Attorney, Agent, or Firm*—Robert P. Blackburn; Barbara G. McClung; Debra A. Shetka[57] **ABSTRACT**

Polynucleotide sequences are provided for the diagnosis of the presence of retroviral infection in a human host associated with lymphadenopathy syndrome and/or acquired immune deficiency syndrome, for expression of polypeptides and use of the polypeptides to prepare antibodies, where both the polypeptides and antibodies may be employed as diagnostic reagents or in therapy, e.g., vaccines and passive immunization. The sequences provide detection of the viral infectious agents associated with the indicated syndromes and can be used for expression of antigenic polypeptides.

22 Claims, 59 Drawing Sheets